

Amendments to the Specification:

Please replace the paragraph beginning at page 4, line 28, with the following amended paragraph:

Figure 3 shows an alignment of the deduced amino acid sequences for the sialyltransferases. The OH4384 *cst-I* gene (first 300 residues) (Cst-I; SEQ ID NO:48), OH4384 *cst-II* gene (OH4384; SEQ ID NO:3) (identical to OH4382 *cst-II*), O:19 (serostrain) *cst-II* gene (O:19; SEQ ID NO:9) (GenBank #AF167344), NCTC 11168 *cst-II* gene (11168; SEQ ID NO:10) and an *H. influenzae* putative ORF (Hi_ORF; SEQ ID NO:49) (GenBank #U32720) were aligned using the ClustalX alignment program (Thompson *et al.* (1997) *Nucleic Acids Res.* **25**, 4876-82). The shading was produced by the program GeneDoc (Nicholas, K. B., and Nicholas, H. B. (1997) URL: <http://www.cris.com/~ketchup/genedoc.shtml>).

Please replace the paragraph (Table 2) beginning at page 48, line 13 with the following amended paragraph:

Table 2: Primers used for Amplification of Open Reading Frames

Primers used to amplify the LPS core biosynthesis locus

CJ42: Primer in heptosylTase-II (SEQ ID NO:40)-(Error! Reference source not found.)

5' GC CAT TAC CGT ATC GCC TAA CCA GG 3' 25 mer

CJ43: Primer in heptosylTase-I (SEQ ID NO:41)-(Error! Reference source not found.)

5' AAA GAA TAC GAA TTT GCT AAA GAG G 3' 25 mer

Primers used to amplify and clone ORF 5a:

CJ-106 (3' primer, 41 mer) (SEQ ID NO:42) ~~(Error! Reference source not found.)~~:

SalI

5' CCT AGG TCG ACT TAA AAC AAT GTT AAG AAT ATT TTT TTT AG 3'

CJ-157 (5' primer, 37 mer) (SEQ ID NO:43) ~~(Error! Reference source not found.)~~:

NdeI

5' CTT AGG AGG TCA TAT GCT ATT TCA ATC ATA CTT TGT G 3'

Primers used to amplify and clone ORF 6a:

CJ-105 (3' primer, 37 mer) (SEQ ID NO:44) ~~(Error! Reference source not found.)~~:

SalI

5' CCT AGG TCG ACC TCT AAA AAA AAT ATT CTT AAC ATT G 3'

CJ-133 (5' primer, 39 mer) (SEQ ID NO:45) ~~(Error! Reference source not found.)~~:

NdeI

5' CTTAGGAGGTCATATGTTTAAATTTCATCATCTTACC 3'

Primers used to amplify and clone ORF 7a:

CJ-131 (5' primer, 41 mer) (SEQ ID NO:46) ~~(Error! Reference source not found.)~~:

NdeI

5' CTTAGGAGGTCATATGAAAAAGTTATTATTGCTGGAAATG 3'

CJ-132 (3' primer, 41 mer) (SEQ ID NO:47) ~~(Error! Reference source not found.)~~:

SalI

5' CCTAGGTCGACTTATTTTCCTTTGAAATAATGCTTTATATC 3'

Amendments to the Informal Sequence Listing:

Please replace the paragraph beginning at page 14, line 1, with the following amended paragraph:

**SEQ. ID NO: 21. Amino acid sequence of β -1,4-GalNAc transferase from *C. jejuni*
~~0:1~~ 0:10.**

Please replace the second paragraph beginning at page 14, line 1, with the following amended paragraph:

**SEQ. ID NO: 22. Nucleotide sequence of β -1,4-GalNAc transferase from *C. jejuni*
~~0:1~~ 0:36.**

Please insert the accompanying paper copy of the Sequence Listing, page numbers 1 to 52, at the end of the application.

In addition, in order to comply with Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Sequence Disclosures, 37 C.F.R. §§ 1.821-1.825, Applicants submit that the computer-readable form in the instant application is identical with that filed in Application No. 10/303,128, filed November 21, 2002, a Divisional of 09/816,028, filed March 21, 2001. In accordance with 37 C.F.R. § 1.821(e), please use the computer-readable form filed in Application No. 09/816,028 (mailed to the PTO on September 6, 2001) as the computer-readable form for the instant application. A paper copy of the last filed Sequence Listing from Application No. 09/816,028 is submitted herewith. The information in the paper copy of the Sequence Listing is identical to that which is in the computer readable form, as required under 37 C.F.R. § 1.821(f).

It is understood that the Patent and Trademark Office will make the necessary changes in application number and filing date for the computer-readable form that will be used for the instant application.

The amendments to the Informal Sequence Listing correct errors of a typographical nature made without deceptive intent. The first corrects the serotype number of C. jejuni of SEQ ID NO:21 from O:1 to O:10 to conform to the nucleotide sequence immediately preceding it, SEQ ID NO:20, and from which it is translated. The second amendment deletes "O:1" from the correct serotype, "O:36", for the nucleotide sequence for SEQ ID NO:22, whose translation product in SEQ ID NO:23 may be found immediately following, with the correct serotype.

Applicants request entry of this amendment in adherence with 37 C.F.R. §§1.821 to 1.825. The information contained in the computer readable form of Application No. 09/816,028 was prepared through the use of the software program "PatentIn" and is identical to that of the paper copy, a copy of which is enclosed for the convenience of the Examiner. This amendment contains no new matter.